Amendments to the Specification:

Please delete the title and replace it with the following:

HUMAN T2R54 TASTE RECEPTOR AND USE FOR IDENTIFYING BITTER TASTE MODULATORS

Please delete the text in paragraph [0060] and replace with the following:

[0060] A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., Nuc. Acids Res., 25:3389-402 (1977) and Altschul et al., J. Mol. Biol., 215:403-10 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., Altschul et al., Nuc. Acids Res., 25:3389-402 (1977) and Altschul et al., J. Mol. Biol., 215 :403-1 0 (1990)). These initial neighborhood-word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always<0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity

and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, PNAS, 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Please delete the text in paragraph [0123] and replace with the following:

[0123] Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) strategy computer program is accessible as and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known taste receptor ligand-binding regions (see. e.g., Rose, Nucleic Acids Res., 26:1628-35 (1998); Singh, Biotechniques, 24:318-19 (1998)).

Please delete the text in paragraph [0132] and replace with the following:

[0132] A chimeric nucleic acid sequence may encode a T2R ligand-binding region within any 7-transmembrane polypeptide. Because 7-transmembrane receptor polypeptides have similar primary sequences and secondary and tertiary structures, structural domains (e.g., extracellular domain, TM. domains, cytoplasmic domain, etc.) can be readily identified by sequence analysis. For ex.ample, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that characterize profiles of the hydrophobicity and variability of analyzed sequences. Periodicity detection enhancement and alpha helical periodicity index can be done as by, e.g., Donnelly, Protein Sci., 2:55-70 (1993). ' Other alignment and modeling algorithms are well known in the art (see. e.g., Peitsch, Receptors Channels, 4:161-64 (1996); Kyte & Doolittle, J. Md. Biol., 157:105-32 (1982); Cronet, Protein Eng., 6:59-64 (1993).